



## SEQUENCE LISTING

&lt;110&gt; ITOH, Iyogo et al.

&lt;120&gt; NOVEL TUMOR ANTIGEN PROTEIN SART-3 AND TUMOR ANTIGEN PEPTIDES THEREOF

&lt;130&gt; 0020-4817P

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&lt;160&gt; 64

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 3798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (12)..(2900)

&lt;223&gt;

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gct gag tcc aag gct ggg ccc aag gct gac gga gag gag gat gag gtt  
Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val  
15 20 25

98

aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct  
Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala  
30 35 40 45

146

gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc  
Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly  
50 55 60

194

gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc gcg gag  
Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu  
65 70 75

242

agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa  
Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Lys  
80 85 90

290

aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc  
Asn Gln Leu Glu Ile Glu Arg Leu Glu Gln Leu Ser Ile Asn Val  
95 100 105

338

tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa  
Tyr Asp Tyr Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu

386

328

110	115	120	125	
ggg gag ctt acc aag gtg agg atg gcc cgc cag aag atg agt gaa atc Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile 130	135	140		434
ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile 145	150	155		482
agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt Ser Met Ala Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe 160	165	170		530
gag aaa gcc gtg aag gat tac att tgt cct aac att tgg cta gag tat Glu Lys Ala Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr 175	180	185		578
ggc cag tac tca gtt ggt ggg att ggt cag aaa ggt ggc ctt gag aaa Gly Gln Tyr Ser Val Gly Ile Gly Gln Lys Gly Leu Glu Lys 190	195	200	205	626
gtt cgc tcc gtg ttt gaa agg gct ctc tcg tct gtt ggt tta cat atg Val Arg Ser Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met 210	215	220		674
acc aaa gga ctc gcc ctc tgg gag gct tac cga gag ttt gaa agt gcg Thr Lys Gly Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala 225	230	235		722
att gtg gaa gct gct cgg ctt gag aaa gtc cac agt ctt ttc cgg cga Ile Val Glu Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg 240	245	250		770
cag ttg gcg atc cca ctc tat gat atg gag gcc aca ttt gca gag tat Gln Leu Ala Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr 255	260	265		818
gaa gaa tgg tca gaa gac cca ata cca gag tca gta att cag aac tat Glu Glu Trp Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr 270	275	280	285	866
aac aaa gca cta cag cag ctg gag aaa tat aaa ccc tat gaa gaa gca Asn Lys Ala Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala 290	295	300		914
ctg ttg cag gca gag gca cca agg ctg gca gaa tat caa gca tat atc Leu Leu Gln Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile 305	310	315		962
gat ttt gag atg aaa att ggc gat cct gct cgc att cag ttg atc ttt Asp Phe Glu Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe 320	325	330		1010
gag cgc gcc ctg gtc gag aac tgc ctt gtc cca gac tta tgg atc cgt Glu Arg Ala Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg 335	340	345		1058

tac agt cag tac cta gat cga caa ctg aaa gta aag gat ttg gtt tta 1106  
 Tyr Ser Gln Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu  
 350 355 360 365  
  
 tct gta cat aac cgc gct att aga aac tgc ccc tgg aca gtt gcc tta 1154  
 Ser Val His Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu  
 370 375 380  
  
 tgg agt cgg tac ctc ttg gcc atg gag aga cat gga gtt gat cat caa 1202  
 Trp Ser Arg Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln  
 385 390 395  
  
 gta att tct gta acc ttc gag aaa gct ttg aat gcc ggc ttc atc cag 1250  
 Val Ile Ser Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln  
 400 405 410  
  
 gcc act gat tat gtg gag att tgg cag gca tac ctt gat tac ctg agg 1298  
 Ala Thr Asp Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg  
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 Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu  
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 agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa 1394  
 Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu  
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 gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac 1442  
 Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn  
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 Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg  
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 gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac 1538  
 Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn  
 495 500 505  
  
 atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag 1586  
 Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln  
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 cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac 1634  
 His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr  
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 cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt 1682  
 Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly  
 545 550 555  
  
 tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta 1730  
 Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu  
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B28

gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala 575 580 585	1778
ctt gtg cag caa gaa gaa aag gct gaa caa cgg aaa aga gct cgg Leu Val Gln Gln Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg 590 595 600 605	1826
gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag Ala Glu Lys Lys Ala Leu Lys Lys Lys Ile Arg Gly Pro Glu 610 615 620	1874
aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu 625 630 635	1922
gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca Glu Glu Gln Pro Ser Lys Arg Arg Val Glu Asn Ser Ile Pro Ala 640 645 650	1970
gct gga gaa aca caa aat gta gaa gta gca gca ggg ccc gct ggg aaa Ala Gly Glu Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys 655 660 665	2018
tgt gct gcc gta gat gtg gag ccc cct tcg aag cag aag gag aag gca Cys Ala Ala Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala 670 675 680 685	2066
gcc tcc ctg aag agg gac atg ccc aag gtg ctg cac gac agc agc aag Ala Ser Leu Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys 690 695 700	2114
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ccg gac acg aag ctc agg cca ctc ttc gag gcc tgt ggg gag gtg gtc Pro Asp Thr Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val 720 725 730	2210
cag atc cga ccc atc ttc agc aac cgt ggg gat ttc cga ggt tac tgc Gln Ile Arg Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys 735 740 745	2258
tac gtg gag ttt aaa gaa gag aaa tca gcc ctt cag gca ctg gag atg Tyr Val Glu Phe Lys Glu Lys Ser Ala Leu Gln Ala Leu Glu Met 750 755 760 765	2306
gac cgg aaa agt gta gaa ggg agg cca atg ttt gtt tcc ccc tgt gtg Asp Arg Lys Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val 770 775 780	2354
gat aag agc aaa aac ccc gat ttt aag gtg ttc agg tac agc act tcc Asp Lys Ser Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser 785 790 795	2402
cta gag aaa cac aag ctg ttc atc tca ggc ctg cct ttc tcc tgt act	2450

Leu Glu Lys His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr  
 800 805 810

aaa gag gaa cta gaa gaa atc tgt aag gct cat ggc acc gtc aag gac 2498  
 Lys Glu Glu Leu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp  
 815 820 825

ctc agg ctg gtc acc aac cgg gct ggc aaa cca aag ggc ctg gcc tac 2546  
 Leu Arg Leu Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr  
 830 835 840 845

gtg gag tat gaa aat gaa tcc cag gcg tcg cag gct gtc atg aag atg 2594  
 Val Glu Tyr Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met  
 850 855 860

gac ggc atg act atc aaa gag aac atc atc aaa gtc gca atc agc aac 2642  
 Asp Gly Met Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn  
 865 870 875

cct cct cag agg aaa gtt cca gag aag cca gag acc agg aag gca cca 2690  
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 880 885 890

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 Gly Gly Pro Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly  
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agg acg cag ctg tct cta ctg cct cgt gcc ctg cag cgc cca agt gct 2786  
 Arg Thr Gln Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala  
 910 915 920 925

gca gct cct cag gct gag aac ggc cct gcc gcg gct cct gca gtt gcc 2834  
 Ala Ala Pro Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala  
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gcc cca gca gcc acc gag gca ccc aag atg tcc aat gcc gat ttt gcc 2882  
 Ala Pro Ala Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala  
 945 950 955

aag ctg ttt ctg aga aag tgaacggac gctggagac aggaaatgcc 2930  
 Lys Leu Phe Leu Arg Lys  
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ttacttcact ctggccggc ggacctccca ccaccagca gtgcactgg gatggacagg 2990

cctggtgtgc tgcgtgctcg caaccacaga tggctcctcg gcttttagaca gaaaggaa 3050

ggggttctaa gtcaagagcc tttcagtgtc ccctcatatt gagggcagtg gcagaaaagt 3110

gaccactctg caggctggc ccaggatgtg gtgtcctgag atagtttgt atctaaaga 3170

ctgaggcaca gaagcgaaac gagaacacac tgttttgag acacagttgt ccaaatttt 3230

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Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Ala Thr Tyr  
35 40 45

Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu  
50 55 60

Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro  
65 70 75 80

Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys Asn Gln Leu  
85 90 95

Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr  
100 105 110

Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu  
115 120 125

Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu

130

135

140

Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile Ser Met Ala  
145 150 155 160

Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe Glu Lys Ala  
165 170 175

Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr Gly Gln Tyr  
180 185 190

Ser Val Gly Gly Ile Gly Gln Lys Gly Gly Leu Glu Lys Val Arg Ser  
195 200 205

Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met Thr Lys Gly  
210 215 220

Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala Ile Val Glu  
225 230 235 240

*Bar*  
Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg Gln Leu Ala  
245 250 255

Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr Glu Glu Trp  
260 265 270

Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr Asn Lys Ala  
275 280 285

Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala Leu Leu Gln  
290 295 300

Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile Asp Phe Glu  
305 310 315 320

Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe Glu Arg Ala  
325 330 335

Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg Tyr Ser Gln  
340 345 350

Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu Ser Val His  
355 360 365

Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu Trp Ser Arg  
370 375 380

Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln Val Ile Ser  
385 390 395 400

Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln Ala Thr Asp  
405 410 415

Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg Arg Arg Val  
420 425 430

Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu Arg Ala Ala  
435 440 445

Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu Glu Arg Phe  
450 455 460

Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn Trp Ala Arg  
465 470 475 480

Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg Glu Leu Trp  
485 490 495

Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn Met Trp Leu  
500 505 510

Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln His Cys Arg  
515 520 525

Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr Pro Glu His  
530 535 540

Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly Ser Leu Glu  
545 550 555 560

Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu Ala Arg Val  
565 570 575

Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala Leu Val Gln  
580 585 590

Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg Ala Glu Lys  
595 600 605

Lys Ala Leu Lys Lys Lys Lys Ile Arg Gly Pro Glu Lys Arg Gly  
610 615 620

Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu Glu Glu Gln  
625 630 635 640

Pro Ser Lys Arg Arg Val Glu Asn Ser Ile Pro Ala Ala Gly Glu  
645 650 655

Thr Gln Asn Val Glu Val Ala Ala Gly Pro Ala Gly Lys Cys Ala Ala  
660 665 670

Val Asp Val Glu Pro Pro Ser Lys Gln Lys Glu Lys Ala Ala Ser Leu  
675 680 685

Lys Arg Asp Met Pro Lys Val Leu His Asp Ser Ser Lys Asp Ser Ile  
690 695 700

Thr Val Phe Val Ser Asn Leu Pro Tyr Ser Met Gln Glu Pro Asp Thr  
705 710 715 720

Lys Leu Arg Pro Leu Phe Glu Ala Cys Gly Glu Val Val Gln Ile Arg  
725 730 735

Pro Ile Phe Ser Asn Arg Gly Asp Phe Arg Gly Tyr Cys Tyr Val Glu  
740 745 750

Phe Lys Glu Glu Lys Ser Ala Leu Gln Ala Leu Glu Met Asp Arg Lys  
755 760 765

Ser Val Glu Gly Arg Pro Met Phe Val Ser Pro Cys Val Asp Lys Ser  
770 775 780

Lys Asn Pro Asp Phe Lys Val Phe Arg Tyr Ser Thr Ser Leu Glu Lys  
785 790 795 800

His Lys Leu Phe Ile Ser Gly Leu Pro Phe Ser Cys Thr Lys Glu Glu  
805 810 815

Leu Glu Glu Ile Cys Lys Ala His Gly Thr Val Lys Asp Leu Arg Leu  
820 825 830

Val Thr Asn Arg Ala Gly Lys Pro Lys Gly Leu Ala Tyr Val Glu Tyr  
835 840 845

Glu Asn Glu Ser Gln Ala Ser Gln Ala Val Met Lys Met Asp Gly Met  
850 855 860

Thr Ile Lys Glu Asn Ile Ile Lys Val Ala Ile Ser Asn Pro Pro Gln  
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Arg Lys Val Pro Glu Lys Pro Glu Thr Arg Lys Ala Pro Gly Gly Pro  
885 890 895

Met Leu Leu Pro Gln Thr Tyr Gly Ala Arg Gly Lys Gly Arg Thr Gln  
900 905 910

Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala Ala Ala Pro  
915 920 925

Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala Ala Pro Ala  
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Leu Arg Lys

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Met Leu Leu Pro Gln Thr Tyr Gly Ala  
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Val Xaa Asp Tyr Asn Cys His Val Asp Xaa  
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Asn Xaa Asn Lys Ala Leu Gln Gln Xaa  
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<400> 56

Ala Xaa Ile Asp Phe Glu Met Lys Xaa  
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Arg Xaa Ala Glu Tyr Gln Ala Tyr Xaa  
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